

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:26:03 ; Search time 29.37 Seconds
(without alignments)
21.991 Million cell updates/second

Title: US-09-331-631A-37
Perfect score: 53

Sequence: 1 CXXCXXXXXXXXXXCXXC 20

1 CXXXXXXXXXXXXXXXXCXXXC 20

Scoring table: BLOSUM62DX

Gapex 10.0 , Gapext 0.5

Searched: 88757 seqs, 32294092 residues

Total number of hits satisfying chosen parameters: 88757

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Minimum DB seq length: 0
Maximum DB seq length: 30000000000
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Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum	Match	100%
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Existing first 45 summaries

Database : SwissProt_39:4

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	52	100.0	43	1	MTA_COIVI	P27086 collinus viri
2	52	100.0	43	1	MTB_COIVI	P27087 collinus viri
3	52	100.0	47	1	THN_PYRPU	P07504 pyrularia p
4	52	100.0	48	1	PIGU_HIRNI	P81499 hirudo nippi
5	52	100.0	48	1	TX26_PHONI	P29425 phonectria
6	52	100.0	49	1	TX25_PHONI	P29424 phonectria
7	52	100.0	55	1	ANTA_HIRME	P80302 hirudo medi
8	52	100.0	55	1	M84C_DROME	Q01444 drosophila
9	52	100.0	56	1	M87E_DROME	P08175 drosophila
10	52	100.0	57	1	GUAM_HIRNI	P46443 hirudo nippi
11	52	100.0	60	1	MTA_SPARU	P52727 speratus aura
12	52	100.0	60	1	MTA_THIECR	P52721 thermarces
13	52	100.0	60	1	MTB_ONCMY	P09862 oncorhynch
14	52	100.0	60	1	MTB_SALSA	P52720 salmo salar
15	52	100.0	60	1	MT_AMBRE	O42152 ambystoma m
16	52	100.0	60	1	MT_BRARE	P527122 brachydanio
17	52	100.0	60	1	MT_CARAU	P527123 carassius a
18	52	100.0	60	1	MT_CHAC	P52724 chanocephala
19	52	100.0	60	1	MT_CYPA	O13369 cyprinus ca
20	52	100.0	60	1	MT_DICIA	Q9P693 dicentrarch
21	52	100.0	60	1	MT_ESOLU	P25127 esox lucius
22	52	100.0	60	1	MT_GADMO	P51802 gadus morhu
23	52	100.0	60	1	MT_ICTRP	O93571 ictalurus p
24	52	100.0	60	1	MT_LITAU	O13357 liza aurata
25	52	100.0	60	1	MT_NOEBA	P25128 noemachellu
26	52	100.0	60	1	MT_OREMO	P52726 oreochromis
27	52	100.0	60	1	MT_PAGRE	Q92145 parogthenia
28	52	100.0	60	1	MT_PARCR	O93450 parachaenic
29	52	100.0	60	1	MT_PERLU	P52725 perca fluvi
30	52	100.0	60	1	MT_PLEPL	P07216 pleuronecte
31	52	100.0	60	1	MT_PSELM	P55345 pseudopleur
32	52	100.0	60	1	MT_RUTRU	P80593 rutilus viv
33	52	100.0	60	1	MT_ZOAVI	P52728 zoarces viv

34	52	100.0	61	1	MTJA_BOVIN	P04356	bos	taurus
35	52	100.0	61	1	MTJA_HORSE	P02800	equus	cabala
36	52	100.0	61	1	MTJA_HUMAN	P04721	homo	sapiens
37	52	100.0	61	1	MTJA_RABBIT	P11957	oryctolagus	
38	52	100.0	61	1	MTJB_HORSE	P02801	equus	cabala
39	52	100.0	61	1	MTJB_HUMAN	P07438	homo	sapiens
40	52	100.0	61	1	MTJB_SHEEP	P09577	ovis	aries
41	52	100.0	61	1	MTJC_SHEEP	P09578	ovis	aries
42	52	100.0	61	1	MTJE_HUMAN	P04732	homo	sapiens
43	52	100.0	61	1	MTJF_HUMAN	P04733	homo	sapiens
44	52	100.0	61	1	MTJG_HUMAN	P13640	homo	sapiens
45	52	100.0	61	1	MTJH_BOVIN	P55942	bos	taurus

ALIGNMENTS

ID	MTA.COLV1	STANDARD:	PRT:	43 AA.
AC	MTA.COLV1			
AC	P27086:			
DT	01-AUG-1992 (rel. 23, Created)			
DT	01-AUG-1992 (rel. 23, Last sequence update)			
DT	01-NOV-1997 (rel. 35, Last annotation update)			
DE	METALLOTHIONEIN A (MTA) (FRAGMENT).			
OC	Colinus virginianus (Bobwhite quail) (common bobwhite).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Archosauria; Aves; Neognathae; Galliformes; Phasianidae;			
OC	Odonotporinae; Colinus.			
RN	(1)			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LIVER;			
RC	MEDLINE=93247066; PubMed=8483164;			
RX	Shattzer K.L., Kage K., Sobieski R.J., Andrews G.K.;			
RA	*Evolution of avian metallothionein: DNA sequence analyses of the			
RT	turkey metallothionein gene and metallothionein cDNAs from pheasant			
RT	and quail.*;			
RL	J. Mol. Evol. 36:255-262(1993).			
CC	-1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE			
CC	RESIDUES THAT BIND VARIOUS HEAVY METALS.			
CC	-1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:			
CC	FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA			
CC	DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLEATE BRIDGES TO 11			
CC	CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE			
CC	BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.			
CC	-1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation			
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL: X62511; CA444370.1; -;			
DR	PIR: S18173; S18173.			
DR	PIR: S33378; S33378.			
DR	PIR: S33380; S33380.			
DR	PIR: S33382; S33382.			
DR	HSSP: P04355; 2MWT.			
DR	INTERPRO: IPR000006; -;			
DR	INTERPRO: IPR003019; -;			
DR	PFAM: PF00131; metalthio. 1.			
DR	PROSITE: PS00203; METALLOTHIONEIN_VET; PARTIAL.			
KW	Metal-binding; Metal-thiolate cluster; Chelation.			
FT	NON_TER	1	16	BETA.
FT	DOMAIN	<1	1	
FT	DOMAIN	17	>43	ALPHA.
FT	METAL	2	2	CLUSTER B.
FT	METAL	6	6	CLUSTER B.
FT	METAL	8	8	CLUSTER B.
FT	METAL	11	11	CLUSTER B.

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FT METAL 13 13 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER A.
FT METAL 21 21 CLUSTER A.
FT METAL 23 23 CLUSTER A.
FT METAL 24 24 CLUSTER A.
FT METAL 28 28 CLUSTER A.
FT METAL 31 31 CLUSTER A.
FT METAL 35 35 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT NON_TER 43 43
SQ SEQUENCE 43 AA: 4401 MW: 1612EB52656EB875 CRC64:

Query Match 100.0%; Score 52; DB 1; Length 43;
Best Local Similarity 20.0%; Pred. No. 43;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXCXXXXXXXXXXCXXC 20
Db 16 CRKSCCSCCPACGNNCKAGC 35

RESULT 2
MTB_COLVI STANDARD: PRT: 43 AA.
AC P27087.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE METALLOTHIONEIN B (MTB) (FRAGMENT).
OS Colinus virginianus (Bobwhite quail) (Common bobwhite).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
OC Odontophorinae; Colinus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=93247066; PubMed=8483164;
RA Shatzker R.L., Kage K., Sobleski R.J., Andrews G.K.;
RT "Evolution of avian metallothionein: DNA sequence analyses of the
RT turkey metallothionein gene and metallothionein cDNAs from pheasant
RT and quail."
RL J. Mol. Evol. 36:255-262(1993).
CC -I- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
CC RESIDUES THAT BIND VARIOUS HEAVY METALS.
CC -I- DOMAIN: CLASS 1 METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
CC -I- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X62512; CAA44371.1; -.
DR PIR: S18174; S18174.
DR PIR: S33379; S33379.
DR HSSP: P04355; 2MRT.
DR INTERPRO: IPR000006; -.
DR PIRAM: PF00131; metalthio; 1.
DR PROSITE: PS00203; METALLOTHIONEIN_VRT; PARTIAL.
KW Metal-binding; Metal-thiolate cluster; Chelation.
FT NON_TER 1 1 BETA
FT DOMAIN <1 16
FT DOMAIN 17 >43 ALPHA.
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FT METAL 2 2 CLUSTER B.
FT METAL 6 6 CLUSTER B.
FT METAL 8 8 CLUSTER B.
FT METAL 11 11 CLUSTER B.
FT METAL 13 13 CLUSTER B.
FT METAL 16 16 CLUSTER B.
FT METAL 20 20 CLUSTER A.
FT METAL 21 21 CLUSTER A.
FT METAL 23 23 CLUSTER A.
FT METAL 24 24 CLUSTER A.
FT METAL 28 28 CLUSTER A.
FT METAL 31 31 CLUSTER A.
FT METAL 35 35 CLUSTER A.
FT METAL 37 37 CLUSTER A.
FT NON_TER 43 43
SQ SEQUENCE 43 AA: 4429 MW: 1612EB40EE6EB875 CRC64:

Query Match 100.0%; Score 52; DB 1; Length 43;
Best Local Similarity 20.0%; Pred. No. 43;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXCXXXXXXXXXXCXXC 20
Db 16 CRKSCCSCCPACGNNCKAGC 35

RESULT 3
THN_PYPYU STANDARD: PRT: 47 AA.
AC P07504.
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 01-JUL-1993 (Rel. 26, Last annotation update)
DE THIONIN.
GN TH1.
OS Pyricularia pubera (Rabbitwood) (Buffalo nut).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Santalales; Santalaceae;
OC Pyricularia.
RN [1]
RP SEQUENCE.
RX MEDLINE=85173323; PubMed=3985614;
RA Vernon L.P., Eveitt G.E., Zeikus R.D., Gray W.R.;
RT "A toxic thionin from Pyricularia pubera: purification, properties, and
RT amino acid sequence."
RL Arch. Biochem. Biophys. 238:18-29(1985).
CC -I- FUNCTION: THIONINS ARE SMALL PLANT PROMEINS WHICH ARE TOXIC
CC TO ANIMAL CELLS. THEY SEEM TO EXERT THEIR TOXIC EFFECT AT THE
CC LEVEL OF THE CELL MEMBRANE. THE PRECISE FUNCTION, IN PLANTS,
CC OF THESE PROTEINS IS NOT KNOWN.
CC -I- SIMILARITY: BELONGS TO THE PLANT THIONIN FAMILY.
CC -----
CC PIR: A24074; A24074.
DR HSSP: P01544; 2PLH.
DR MENDEL: 13438; PYPYU; TH1.3.
DR INTERPRO: IPR001010; -.
DR PIRAM: PF00321; plant_thionins; 1.
DR PROSITE: PS00287; THIONIN.
DR PROSITE: PS00271; THIONIN; 1.
KW Thionin; Plant toxin.
FT DISULFID 3 41 BY SIMILARITY.
FT DISULFID 4 31 BY SIMILARITY.
FT DISULFID 16 27 BY SIMILARITY.
SQ SEQUENCE 47 AA: 5288 MW: 87E10460D8E4C6E1 CRC64:

Query Match 100.0%; Score 52; DB 1; Length 47;
Best Local Similarity 20.0%; Pred. No. 45;
Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CXXXCXXXXXXXXXXCXXC 20
Db 12 CYNCRPLPPTTSRETCARKC 31
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RESULT 4
 ID PIGU_HIRNI STANDARD; PRT: 48 AA.
 AC P81459;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE PIGUMERIN.
 OS Hirudo nipponia.
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=98351570; PubMed=9688284;
 RA Kim D.R., Kang K.W.;
 RT "Amino acid sequence of pigumerin, an antistasin-type protease
 inhibitor from the blood sucking leech Hirudo nipponia.";
 RL Eur. J. Biochem. 254:692-697(1998).
 CC -1- FUNCTION: INHIBITS PLASMA AND TISSUE KALLIKREIN, AND TRYPSIN. MAY
 BE INVOLVED IN LEECH HEMATOPHAGIA.
 CC -1- SIMILARITY: BELONGS TO THE ANTISTASIN FAMILY.
 CC Serine protease inhibitor.
 KW ACT_SITE 27 28 REACTIVE_BOND.
 FT DISULFID 3 14 BY SIMILARITY.
 FT DISULFID 8 19 BY SIMILARITY.
 FT DISULFID 21 41 BY SIMILARITY.
 FT DISULFID 26 45 BY SIMILARITY.
 FT DISULFID 30 47 BY SIMILARITY.
 SQ SEQUENCE 48 AA; 5101 MW; 0331C2D807F32FDC CRC64;

Query Match 100.0%; Score 52; DB 1; Length 48;
 Best Local Similarity 20.0%; Pred. No. 46;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXC 20
 |:::|:::|:::|:::|:::|
 Db 26 CRKXCPNGFKKDCGCTFPC 45

RESULT 5
 ID TX26_PHONI STANDARD; PRT: 48 AA.
 AC P29425;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-APR-1993 (Rel. 25, Last annotation update)
 DE NEUROTOXIN TX2-6.
 OS Phoneutria nigriventer (Brazilian armed spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-VENOM;
 RX MEDLINE=93011905; PubMed=1397265;
 RA Cordeliro M.N., Diniz C.R., Valentim A.C., von Eickstedt V.R.D.,
 RA Gilroy J., Richardson M.;
 RT "The purification and amino acid sequences of four Tx2 neurotoxins
 from the venom of the Brazilian 'armed' spider Phoneutria nigriventer
 (Keys).";
 RL FEBS Lett. 310:153-156(1992).
 CC -1- FUNCTION: CAUSES SCRATCHING, LACRIMATION, HYPERSALIVATION,
 SWEATING AND AGITATION FOLLOWED BY SPASTIC PARALYSIS OF THE
 ANTERIOR AND POSTERIOR EXTREMITIES AND DEATH AT DOSE LEVELS OF
 0.79 MG/MOUSE. IT SIGNIFICANTLY ACTIVATES VOLTAGE-DEPENDENT SODIUM
 CHANNELS. INSECTICIDAL TO THE LARVAL AND ADULT FORMS OF THE HOUSE
 FLY.
 CC -1- SIMILARITY: TO NEUROTOXINS TX2-1 AND TX2-5.
 CC PIR: S29216; S29216.
 KW Venom; Neurotoxin.
 SQ SEQUENCE 48 AA; 5298 MW; 4F30FBFCE4919CD CRC64;

Query Match 100.0%; Score 52; DB 1; Length 48;
 Best Local Similarity 20.0%; Pred. No. 46;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXC 20
 |:::|:::|:::|:::|:::|
 Db 10 CKETCDCCGERGECVCGPC 29

RESULT 6
 ID TX25_PHONI STANDARD; PRT: 49 AA.
 AC P29424;
 DT 01-APR-1993 (Rel. 25, Created)
 DT 01-APR-1993 (Rel. 25, Last sequence update)
 DT 01-JUL-1993 (Rel. 26, Last annotation update)
 DE NEUROTOXIN TX2-5.
 OS Phoneutria nigriventer (Brazilian armed spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Entelegynae; Lycosoidea; Ctenidae; Phoneutria.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-VENOM;
 RX MEDLINE=93011905; PubMed=1397265;
 RA Cordeliro M.N., Diniz C.R., Valentim A.C., von Eickstedt V.R.D.,
 RA Gilroy J., Richardson M.;
 RT "The purification and amino acid sequences of four Tx2 neurotoxins
 from the venom of the Brazilian 'armed' spider Phoneutria nigriventer
 (Keys).";
 RL FEBS Lett. 310:153-156(1992).
 RN [2]
 RP SEQUENCE OF 1-10.
 RC TISSUE-VENOM;
 RX MEDLINE=92196803; PubMed=1801316;
 RA Rezende L. Jr., Cordeliro M.N., Oliveira E.B., Diniz C.R.;
 RT "Isolation of neurotoxic peptides from the venom of the 'armed'
 spider Phoneutria nigriventer.";
 RL Toxicon 29:1225-1233(1991).
 CC -1- FUNCTION: CAUSES SCRATCHING, LACRIMATION, HYPERSALIVATION,
 SWEATING AND AGITATION FOLLOWED BY SPASTIC PARALYSIS OF THE
 ANTERIOR AND POSTERIOR EXTREMITIES AND DEATH AT DOSE LEVELS OF
 0.24 MG/MOUSE. INSECTICIDAL TO THE LARVAL AND ADULT FORMS OF THE
 HOUSE FLY.
 CC -1- SIMILARITY: TO NEUROTOXINS TX2-1 AND TX2-6.
 CC PIR: B39305; B39305.
 DR PIR: S29215; S29215.
 KW Venom; Neurotoxin.
 SQ SEQUENCE 49 AA; 5111 MW; 77B46AAB3911716 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 49;
 Best Local Similarity 20.0%; Pred. No. 46;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

QY 1 CXXXXXXXXXXXXXXXXC 20
 |:::|:::|:::|:::|:::|
 Db 10 CKVTCDCCGERGECVCGPC 29

RESULT 7
 ID ANTA_HIRME STANDARD; PRT: 55 AA.
 AC P80302;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE HIRUSTASIN.
 OS Hirudo medicinalis (medicinal leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
 OC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
 RN [1]

GN MST(3)Gt-9 OR MST87F.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CANTON-S;
 RA MEDLINE=88211557; PubMed=2835228;
 RA Kuhn R., Schaefer U., Schaefer M.;
 RT "Cis-acting regions sufficient for spermatocyte-specific
 RT transcriptional and spermatid-specific translational control of the
 RT Drosophila melanogaster gene mst(3)91-9.";
 RN EMBO J. 7:447-454(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanalides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abail J.F., Agayari A., An H.-J., Andrews-Plannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dletz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleeb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 CC -I- TISSUE SPECIFICITY: TESTIS.
 CC -I- DEVELOPMENTAL STAGE: PRIMARY SPERMATOCYTES.
 CC -I- DOMAIN: THIS PROTEIN IS MOSTLY COMPOSED OF REPEPTITIVE C-G-P
 CC MOTIFS.
 CC -I- SIMILARITY: BELONGS TO THE MST(3)CGP FAMILY.
 CC -----
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 CC -----
 CC DR EMBL: Y00831; CAA68761.1; -.
 CC DR EMBL: AE003702; AAF54994.1; -.
 CC DR PIR: S00340; WTEF.

DR HSPB; P01180; INPO.
 DR FLYBASE; FBgn0002862; Mst87F.
 KW Spermatogenesis; Repeat; Multigene family.
 SQ SEQUENCE 56 AA; 5233 MW; 830CD13212C34A47 CRC64;
 Query Match 100.0%; Score 52; DB 1; Length 56;
 Best Local Similarity 20.0%; Pred. No. 51;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CXXXKXXXXXXXXXXCXXC 20
 DB 2 CCGPCGPGCCGPGCCGPGC 21
 RESULT 10
 ID GUAM_HIRNT STANDARD; PRT; 57 AA.
 AC P46443;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GUAMERIN.
 OS Hirudo nipponia.
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudiniida; Hirudinea;
 OC Arynchobdellida; Hirudiniiformes; Hirudiniidae; Hirudo.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95293987; PubMed=7775446;
 RA Jung H.I., Kim S.I., Ha K.S., Joe C.O., Kang K.W.;
 RT "Isolation and characterization of guamerin, a new human leukocyte
 RT elastase inhibitor from Hirudo nipponia.";
 RL J. Biol. Chem. 270:13879-13884(1995).
 CC -I- FUNCTION: INHIBITS MAMMALIAN ELASTASES.
 CC -I- TISSUE SPECIFICITY: NOT FOUND IN THE SALIVA, BUT IN THE BODY
 CC TISSUES.
 CC -----
 CC -I- SIMILARITY: BELONGS TO THE ANTISTASIN FAMILY.
 CC DR HSPB; P80302; IHIA.
 DR Serine protease inhibitor.
 FT ACT SITE 36 37 REACTIVE BOND.
 FT DISULFID 12 23 BY SIMILARITY.
 FT DISULFID 17 28 BY SIMILARITY.
 FT DISULFID 30 50 BY SIMILARITY.
 FT DISULFID 35 54 BY SIMILARITY.
 FT DISULFID 39 56 BY SIMILARITY.
 SQ SEQUENCE 57 AA; 6123 MW; C5118B6E5481D7B CRC64;
 Query Match 100.0%; Score 52; DB 1; Length 57;
 Best Local Similarity 20.0%; Pred. No. 51;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 OY 1 CXXXKXXXXXXXXXXCXXC 20
 DB 35 CMIFCPNGKGVDENGCEYPC 54
 RESULT 11
 ID MTA_SPAU STANDARD; PRT; 60 AA.
 AC P52727;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE METALLOTHIONEIN A (MT A).
 OS Sparus aurata (Gilthead sea bream).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Acanthopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
 OC Sparidae; Sparus.
 RN [1]
 RP SEQUENCE FROM N.A.

QY 1 CXXXXXXXXXXXXXXC 20
 ID P09862; STANDARD; PRT; 60 AA.
 DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE METALLOTHIONEIN B (Mt-B).
 GN MTB.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), and
 OS Salvelinus alpinus (Arctic char).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC SPECIES=O.MYKISS; PubMed=2448099;
 RX MEDLINE=88111026; PubMed=2448099;
 RA Bonham K., Zafarullah M., Gedamu L.;
 RT "The rainbow trout metallothioneins: molecular cloning and
 RL characterization of two distinct cDNA sequences.";
 RN DNA 6:519-528(1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC SPECIES=O.MYKISS;
 RX MEDLINE=89039876; PubMed=3185557;
 RA Zafarullah M., Bonham K., Gedamu L.;
 RT "Structure of the rainbow trout metallothionein B gene and
 RL characterization of its metal-responsive region.";
 RN Mol. Cell. Biol. 8:4469-4476(1988).
 RL [3]
 RP SEQUENCE FROM N.A.
 RC SPECIES=O.MYKISS; TISSUE=LIVER;
 RX MEDLINE=91316146; PubMed=1859844;
 RA Kille P., Stephens P.E., Kay J.;
 RT "Elucidation of cDNA sequences for metallothioneins from rainbow
 RT trout, stone loach and pike liver using the polymerase chain
 RT reaction.";
 RL Biochim. Biophys. Acta 1089:407-410(1991).
 RL [4]
 RP SEQUENCE FROM N.A.
 RC SPECIES=S.ALPINUS; TISSUE=LIVER;
 RA Gerpe M., Kling P., Olsson P.E.;
 RT "Metallothionein cDNA sequences and gene expression in arctic char
 RT (Salvelinus alpinus) following metal and PCB exposure.";
 RL Mar. Environ. Res. 46:551-554(1998).
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
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 CC -----
 CC EMBL; M18104; AAA49566.1; -
 CC EMBL; M22487; AAA49567.1; -
 CC EMBL; X59394; CAA42037.1; -
 CC EMBL; AF013801; AAB6643.1; -

DR PIR; A30818; A30818.
 DR PIR; B27490; B27490.
 DR PIR; S16997; S16997.
 DR PIR; S15509; S15509.
 DR HSSP; P04355; 2MR.
 DR INTERPRO; IPR000006; -
 DR INTERPRO; IPR003019; -
 DR PFAM; PF00131; metalthio; 1.
 DR PRINTS; PR00860; MTVEPTEBRATE.
 DR PROSITE; PS00203; METALLOTHIONEIN VRT; 1.
 KW Metal-binding; Metal-thiolate cluster; Chelation.
 FT DOMAIN 1 28
 FT 29 60
 FT METAL 4 4
 FT METAL 6 6
 FT METAL 12 12
 FT METAL 14 14
 FT METAL 18 18
 FT METAL 20 20
 FT METAL 23 23
 FT METAL 25 25
 FT METAL 28 28
 FT METAL 32 32
 FT METAL 33 33
 FT METAL 35 35
 FT METAL 36 36
 FT METAL 40 40
 FT METAL 43 43
 FT METAL 47 47
 FT METAL 49 49
 FT METAL 54 54
 FT METAL 58 58
 FT METAL 59 59
 SQ SEQUENCE 60 AA; 6033 MW; 9EA1E70FBE59B4EE CRC64;
 Query Match 100.0%; Score 52; DB 1; Length 60;
 Best local Similarity 20.0%; Pred. No. 53;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CXXXXXXXXXXXXXXC 20
 ID P52720; STANDARD; PRT; 60 AA.
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE METALLOTHIONEIN B (Mt-B).
 GN MTB.
 OS Salmo salar (Atlantic salmon).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LIVER;
 RA Kille P., Olsson P.E.;
 RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS (BY SIMILARITY).
 CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVALENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO 11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVALENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.
 CC -----
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CC EMBL: X97275; CAA65930.1; -
 DR HSSP: P18055; 1MRB.
 DR INTERPRO: IPR000006; -
 DR INTERPRO: IPR003019; -
 DR PFAM: PF00131; metalchio; 1.
 DR PRINTS: PRO0860; MTVERTERATE.
 DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-thiolate cluster; Chelation.

FT DOMAIN 1 28 ALPHA.
 FT METAL 29 60
 FT METAL 4 4 CLUSTER B.
 FT METAL 6 6 CLUSTER B.
 FT METAL 12 12 CLUSTER B.
 FT METAL 14 14 CLUSTER B.
 FT METAL 18 18 CLUSTER B.
 FT METAL 20 20 CLUSTER B.
 FT METAL 23 23 CLUSTER B.
 FT METAL 25 25 CLUSTER B.
 FT METAL 28 28 CLUSTER B.
 FT METAL 32 32 CLUSTER A.
 FT METAL 33 33 CLUSTER A.
 FT METAL 35 35 CLUSTER A.
 FT METAL 36 36 CLUSTER A.
 FT METAL 40 40 CLUSTER A.
 FT METAL 43 43 CLUSTER A.
 FT METAL 47 47 CLUSTER A.
 FT METAL 49 49 CLUSTER A.
 FT METAL 54 54 CLUSTER A.
 FT METAL 58 58 CLUSTER A.
 FT METAL 59 59 CLUSTER A.
 SQ SEQUENCE 60 AA: 5959 MW: 187A9D0FBESBD967 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 60;
 Best Local Similarity 20.0%; Pred. No. 53;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXXXXXXXXXXXXCXXC 20
 I:::|:::|:::|:::|:::|
 DB 28 CKKSCCPCPCGSCGSCASC 47

RESULT 15
 ID MT_AMBME STANDARD: PRT; 60 AA.
 AC 042152;
 DT 01-OCT-2000 (Rel. 40, Created)
 DT 01-OCT-2000 (Rel. 40, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE METALLOTHIONEIN (MT).
 GN MT-A.
 OS Ambystoma mexicanum (Axiolotl).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Ambystomidae;
 OC Ambystoma.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-EMBRYO;
 RA Saint-Jacques E., Guay J., Wirtanen L., Huard V., Stewart G.,
 RA Seguin C.;
 RT "Cloning of a complementary DNA encoding an Ambystoma mexicanum
 RT metallothionein, AmMT-A, and expression of the gene during early
 RT development."
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: METALLOTHIONEINS HAVE A HIGH CONTENT OF CYSTEINE
 CC RESIDUES THAT BIND VARIOUS HEAVY METALS.

CC -1- DOMAIN: CLASS I METALLOTHIONEINS CONTAIN 2 METAL-BINDING DOMAINS:
 CC FOUR DIVERGENT IONS ARE CHELATED WITHIN CLUSTER A OF THE ALPHA
 CC DOMAIN AND ARE COORDINATED VIA CYSTEINYL THIOLATE BRIDGES TO-11
 CC CYSTEINE LIGANDS. CLUSTER B, THE CORRESPONDING REGION WITHIN THE
 CC BETA DOMAIN, CAN LIGATE THREE DIVERGENT IONS TO 9 CYSTEINES.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 IN METALLOTHIONEIN SUPERFAMILY.

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CC EMBL: AF008583; AAB71835.1; -
 DR HSSP: P04355; 2MRP.
 DR INTERPRO: IPR000006; -
 DR INTERPRO: IPR003019; -
 DR PFAM: PF00131; metalchio; 1.
 DR PRINTS: PRO0860; MTVERTERATE.
 DR PROSITE: PS00203; METALLOTHIONEIN_VRT; 1.
 KW Metal-binding; Metal-thiolate cluster; Chelation.

FT DOMAIN 1 28 ALPHA.
 FT METAL 29 60
 FT METAL 3 3 CLUSTER B.
 FT METAL 5 5 CLUSTER B.
 FT METAL 11 11 CLUSTER B.
 FT METAL 13 13 CLUSTER B.
 FT METAL 17 17 CLUSTER B.
 FT METAL 19 19 CLUSTER B.
 FT METAL 22 22 CLUSTER B.
 FT METAL 24 24 CLUSTER B.
 FT METAL 27 27 CLUSTER B.
 FT METAL 31 31 CLUSTER A.
 FT METAL 32 32 CLUSTER A.
 FT METAL 34 34 CLUSTER A.
 FT METAL 35 35 CLUSTER A.
 FT METAL 39 39 CLUSTER A.
 FT METAL 42 42 CLUSTER A.
 FT METAL 46 46 CLUSTER A.
 FT METAL 48 48 CLUSTER A.
 FT METAL 56 56 CLUSTER A.
 FT METAL 58 58 CLUSTER A.
 FT METAL 59 59 CLUSTER A.
 SQ SEQUENCE 60 AA: 5979 MW: AB05F49153953279 CRC64;

Query Match 100.0%; Score 52; DB 1; Length 60;
 Best Local Similarity 20.0%; Pred. No. 53;
 Matches 4; Conservative 16; Mismatches 0; Indels 0; Gaps 0;

OY 1 CXXXXXXXXXXXXXXCXXC 20
 I:::|:::|:::|:::|:::|
 DB 27 CKKSCCPCPCGSCGSCGSC 46

Search completed: March 1, 2001, 16:26:03
 Job time: 400 sec